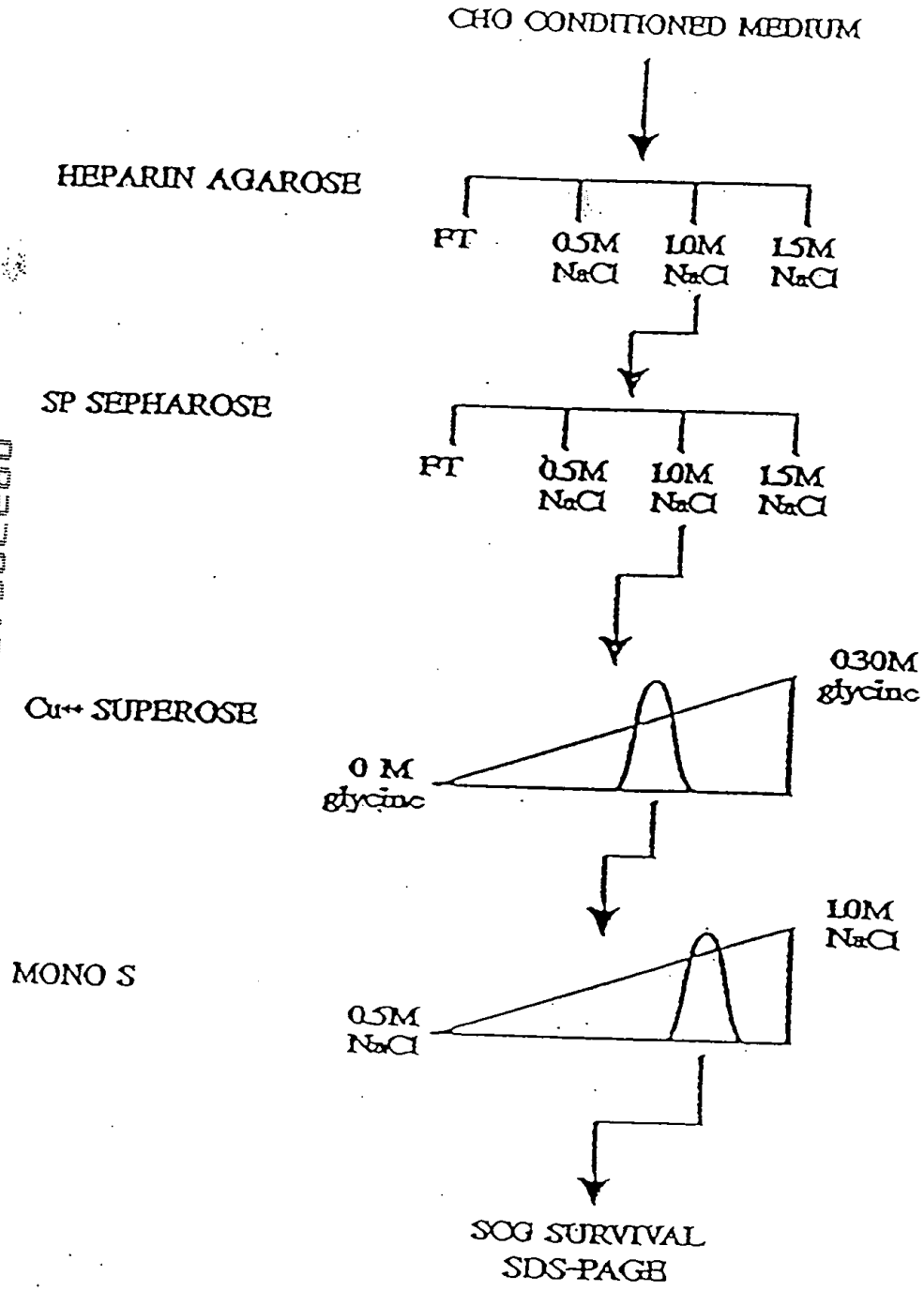


Figure 1

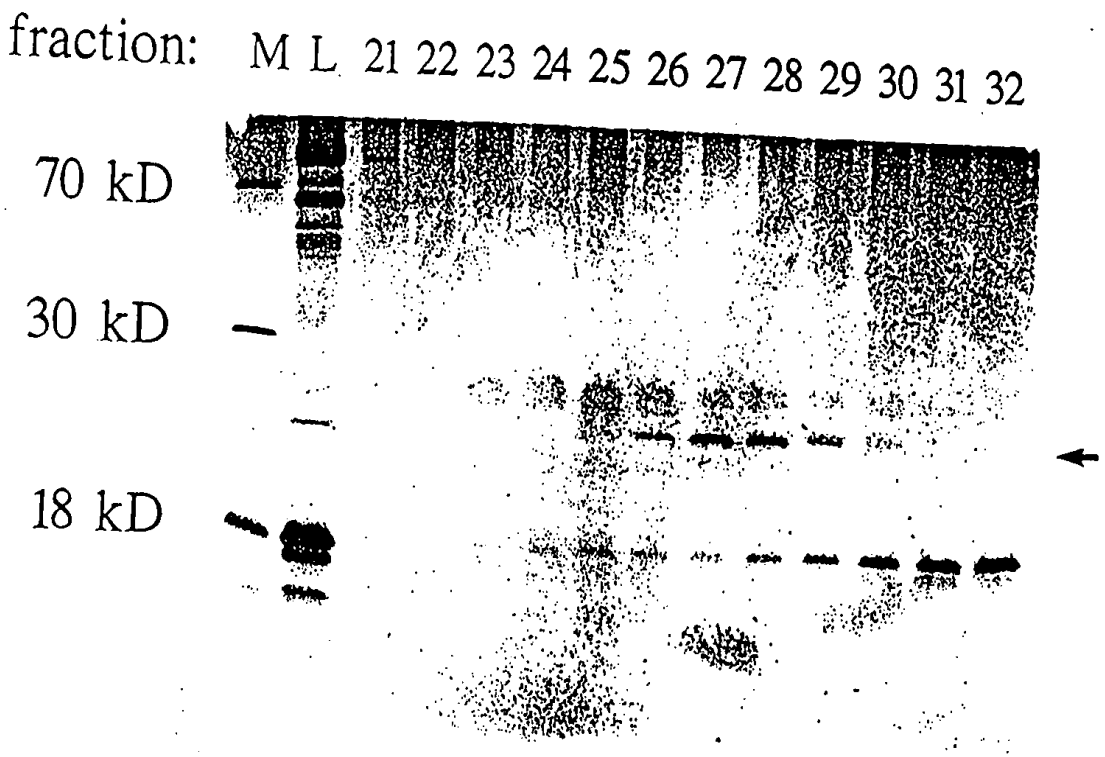
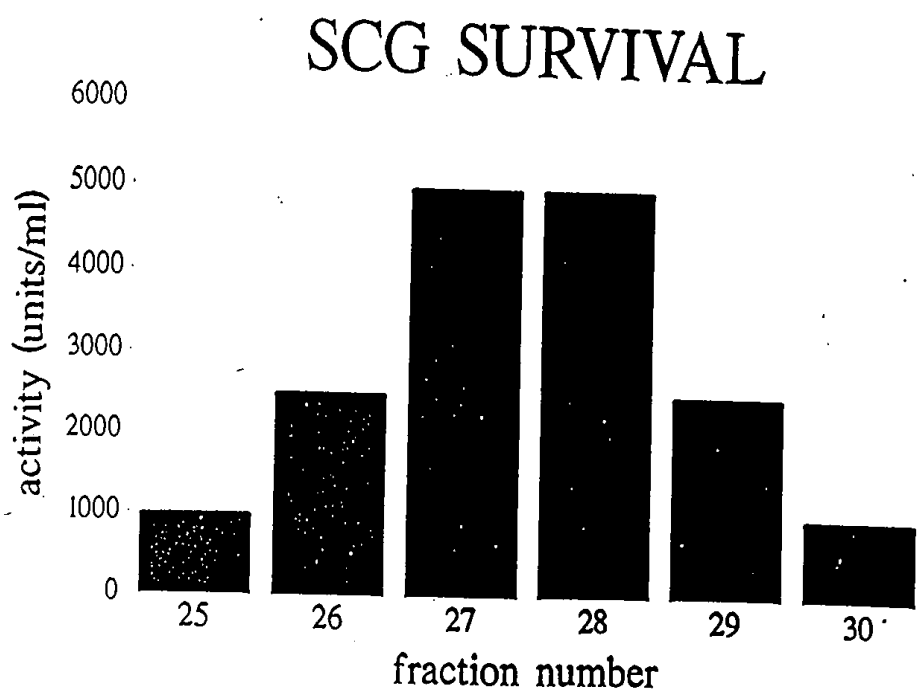


Figure 2a



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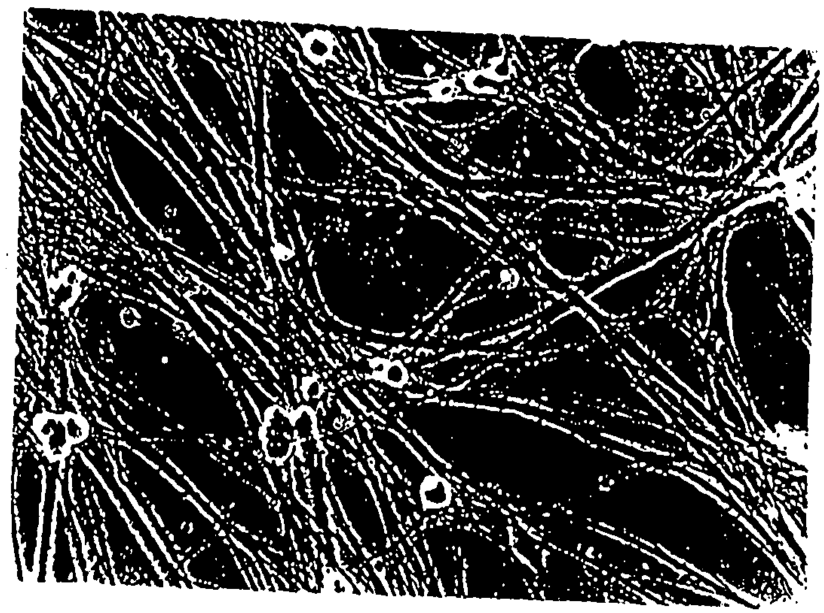


Figure 3a NGF

Figure 3b Anti-NGF

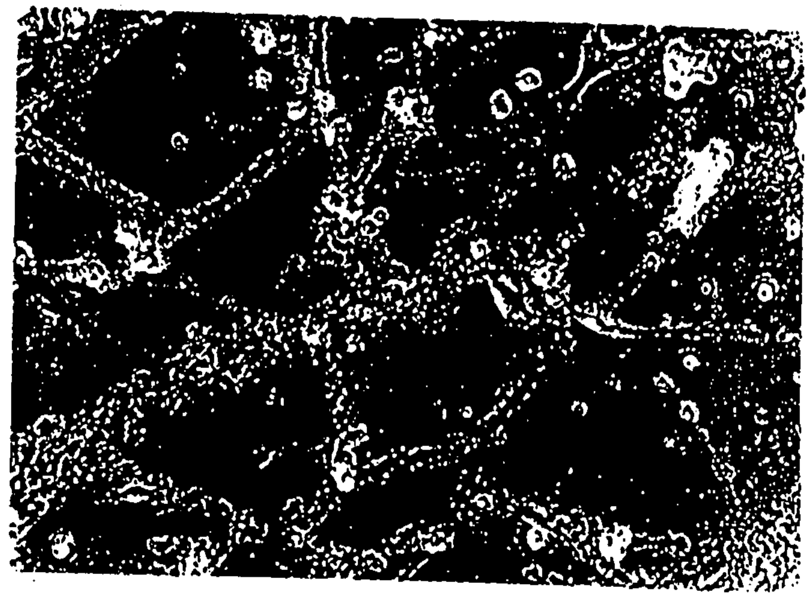
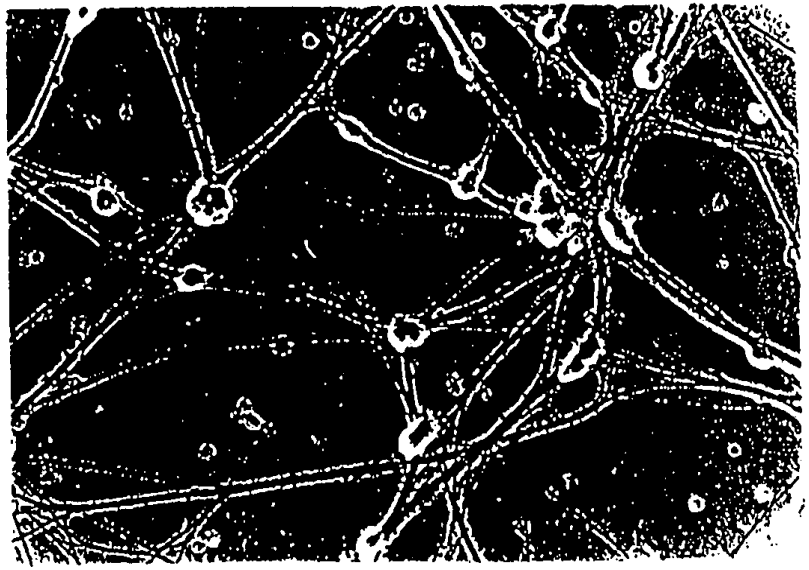


Figure 3c Anti-NGF
+
Neurturin



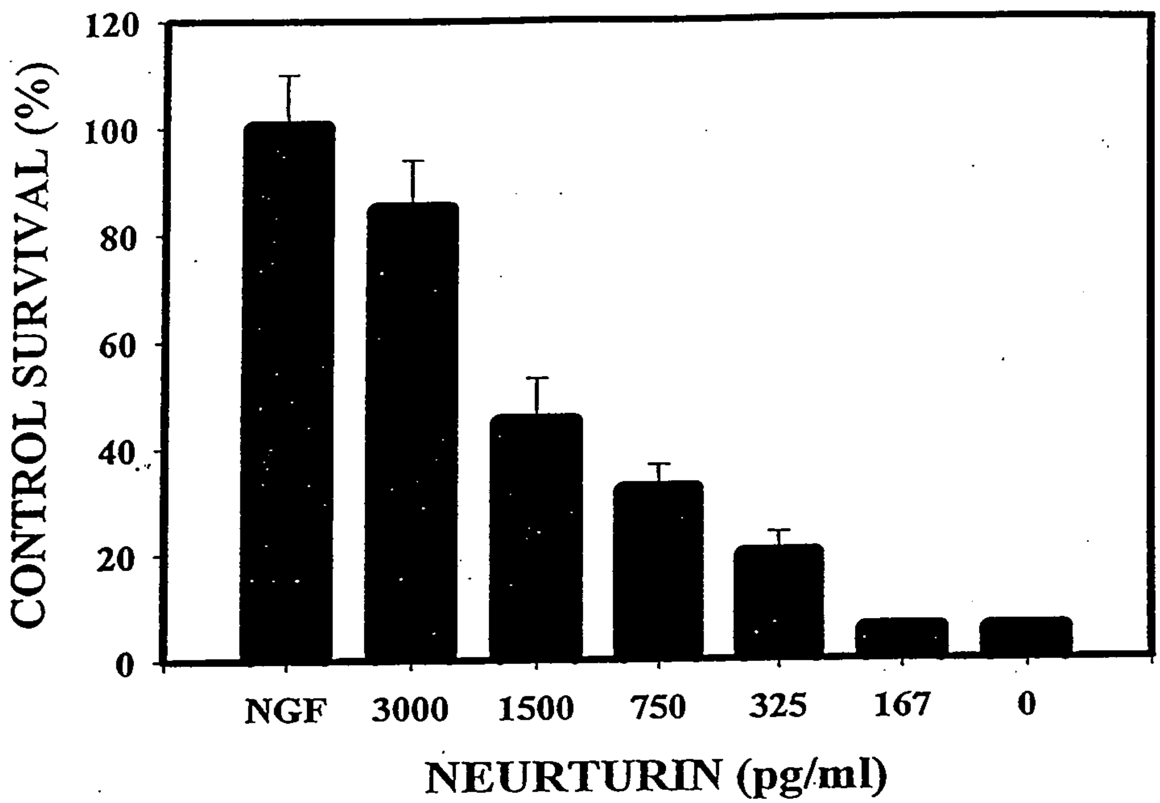
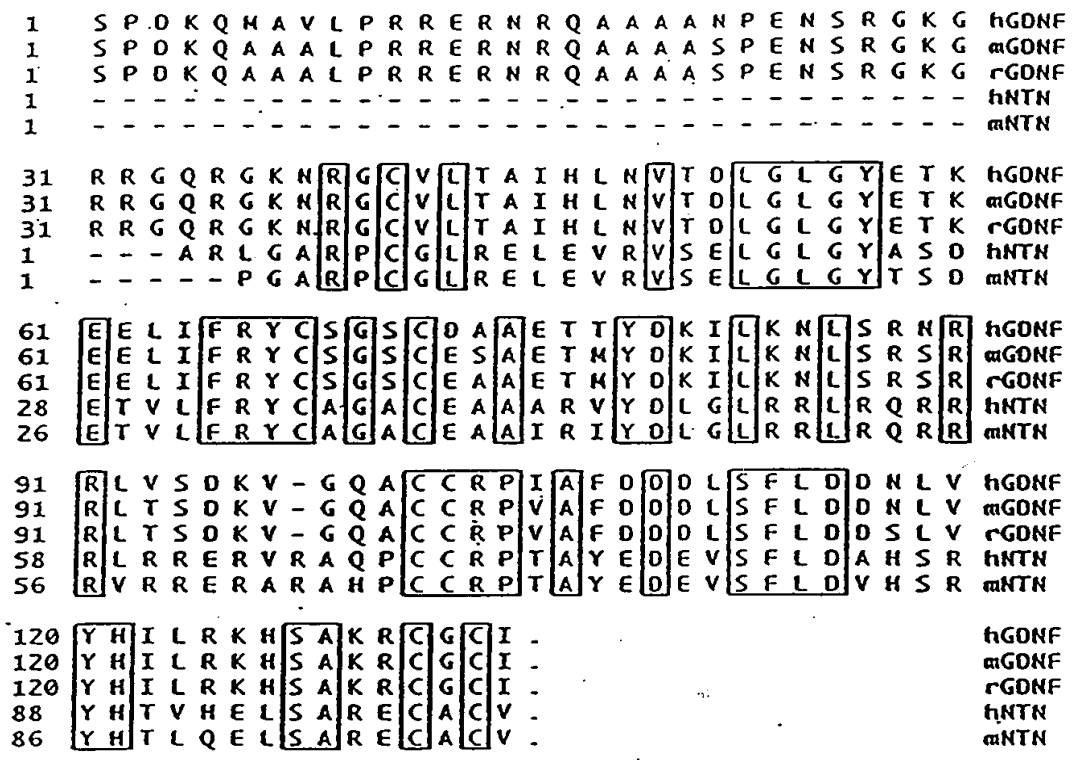


Figure 4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1 S P D K Q A A A L P R R E R N R Q A A A A S P E N S R G K G mGDNF
1 S P D K Q A A A L P R R E R N R Q A A A A S P E N S R G K G rGDNF
1 - hNTN
1 - mNTN
31 R R G Q R G K N R G C V L T A I H L N V T D L G L G Y E T K hGDNF
31 R R G Q R G K N R G C V L T A I H L N V T D L G L G Y E T K mGDNF
31 R R G Q R G K N R G C V L T A I H L N V T D L G L G Y E T K rGDNF
1 - - - A R L G A R P C G L R E L E V R V S E L G L G Y A S D hNTN
1 - - - - - P G A R P C G L R E L E V R V S E L G L G Y T S D mNTN
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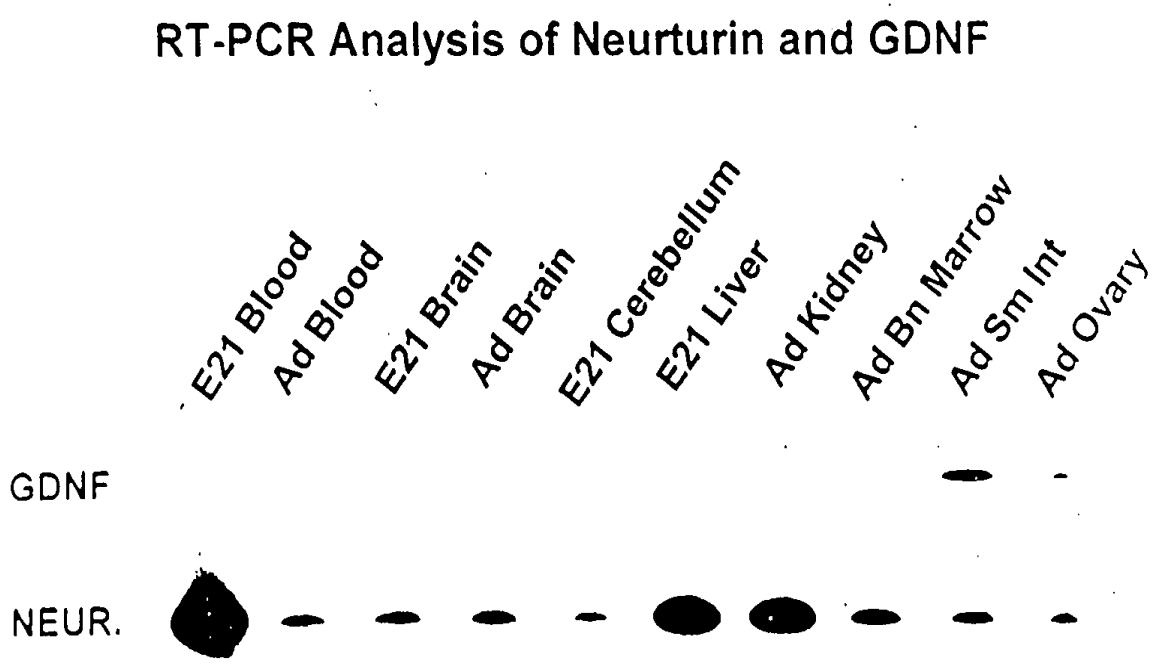
61 E E L I F R Y C S G S C E S A E T M Y D K I L K N L S R S R mGDNF
61 E E L I F R Y C S G S C E A A E T M Y D K I L K N L S R S R rGDNF
28 E T V L F R Y C A G A C E A A A R V Y D L G L R R L R Q R R hNTN
26 E T V L F R Y C A G A C E A A I R I Y D L G L R R L R Q R R mNTN
91 R L V S D K V - G Q A C C R P I A F D D D L S F L D D N L V hGDNF
91 R L T S D K V - G Q A C C R P V A F D D D L S F L D D N L V mGDNF
91 R L T S D K V - G Q A C C R P V A F D D D L S F L D D S L V rGDNF
58 R L R R E R V R A Q P C C R P T A Y E D E V S F L D A H S R hNTN
56 R V R R E R A R A H P C C R P T A Y E D E V S F L D V H S R mNTN
120 Y H I L R K H S A K R C G C I . hGDNF
120 Y H I L R K H S A K R C G C I . mGDNF
120 Y H I L R K H S A K R C G C I . rGDNF
88 Y H T V H E L S A R E C A C V . hNTN
86 Y H T L Q E L S A R E C A C V . mNTN

Figure 5

Figure 6



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Trp Met Cys Arg Glu Gly Leu Leu Leu Ser His Arg Leu Gly Pro Ala Leu Val Pro Leu

CACCGCCTGCCTCGAACCCTGGACGCCCGGATTGCCCGCCTGGCCCAGTACCGTGCACTC 180
His Arg Leu Pro Arg Thr Leu Asp Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu

CTGCAGGGGGCCCCGGATGCGATGGAGCTGCGCGAGCTGACGCCCTGGGCTGGGCGGCCC 240
Leu Gln Gly Ala Pro Asp Ala Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro

CCAGGTCCGCGCCGTCGGGCGGGGCCCCGGCGGCGGCGCGCGTGCGCGGTTGGGGGCG 300
Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg Ala Arg Leu Gly Ala

CGGCCTTGCGGGCTGCGCGAGCTGGAGGTGCGCGTGAGCGAGCTGGGCCTGGGCTACGCG 360
Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu Leu Gly Leu Gly Tyr Ala

TCCGACGAGACGGTGCTGTTCCGCTACTGCGCAGGCGCCTGCGAGGCTGCCGCGCGCGTC 420
Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val

TACGACCTCGGGCTGCGACGACTGCGCCAGCGGCGGCGCCTGCGGCGGGAGCGGGTGCGC 480
Tyr Asp Leu Gly Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg Val Arg

GCGCAGCCCTGCTGCCGCCCGACGGCCTACGAGGACGAGGTGTCCTTCCTGGACGCGCAC 540
Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp Ala His

AGCCGCTACCACACGGTGCACGAGCTGTCGGCGCGCGAGTGCGCCTGCGTGTGA 594
Ser Arg Tyr His Thr Val His Glu Leu Ser Ala Arg Glu Cys Ala Cys Val

Figure 7

```
ATGAGGCGCTGGAAGGCAGCGGCCCTGGTGTCGCTCATCTGCAGCTCCCTGCTATCTGTC  60
Met Arg Arg Trp Lys Ala Ala Ala Leu Val Ser Leu Ile Cys Ser Ser Leu Leu Ser Val

TGGATGTGCCAGGAGGGTCTGCTCTTGGGCCACCGCCTGGGACCCGCGCTTGCCCCGCTA  120
Trp Met Cys Gln Glu Gly Leu Leu Leu Gly His Arg Leu Gly Pro Ala Leu Ala Pro Leu

CGACGCCCTCCACGCACCCTGGACGCCCGCATCGCCCGCCTGGCCCAGTATCGCGCTCTG  180
Arg Arg Pro Pro Arg Thr Leu Asp Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu

CTCCAGGGCGCCCCCGACGCGGTGGAGCTTCGAGAACTTTCTCCCTGGGCTGCCCGCATC  240
Leu Gln Gly Ala Pro Asp Ala Val Glu Leu Arg Glu Leu Ser Pro Trp Ala Ala Arg Ile

CCGGGACCGCGCCGTCGAGCGGGTCCCCGGCGTCGGCGGCGCGGCCGGGGGCTCGGCCT  300
Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg Pro Gly Ala Arg Pro

TGTGGGCTGCGCGAGCTCGAGGTGCGCGTGAGCGAGCTGGGCCTGGGCTACACGTCGGAT  360
Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu Leu Gly Leu Gly Tyr Thr Ser Asp

GAGACCGTGCTGTTCCGCTACTGCGCAGGCGCGTGCGAGGCGGCCATCCGCATCTACGAC  420
Glu Thr Val Leu Phe Arg Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ile Arg Ile Tyr Asp

CTGGGCCTTCGGCGCCTGCGCCAGCGGAGGCGCGTGCGCAGAGAGCGGGCGCGGGCGCAC  480
Leu Gly Leu Arg Arg Leu Arg Gln Arg Arg Arg Val Arg Arg Glu Arg Ala Arg Ala His

CCGTGTTGTCGCCCGACGGCCTATGAGGACGAGGTGTCCTTCCTGGACGTGCACAGCCGC  540
Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp Val His Ser Arg

TACCACACGCTGCAAGAGCTGTCGGCGCGGGAGTGCGCGTGCGTGTGA  588
Tyr His Thr Leu Gln Glu Leu Ser Ala Arg Glu Cys Ala Cys Val  *
```

Figure 8

GGAGGGAGAGCGCGGTGGTTTCGTCCGTGTGCCCCGCGCCCGGCGC -301
TCCTCGCGTGGCCCCGCGTCCTGAGCGCGCTCCAGCCTCCCACGCGCGCC -251
ACCCCGGGGTTCACTGAGCCCGGCGAGCCCGGGGAAGACAGAGAAAGAGA -201
GGCCAGGGGGGGAACCCCATGGCCCGGCCCGTGTCCCGCACCCTGTGCGG -151
TGGCCTCCTCCGGCACGGGGTCCCCGGGTCGCCTCCGGTCCCCGCGATCC -101
GGATGGCGCACGCAGTGGCTGGGGCCGGGCCGGGCTCGGGTGGTCGGAGG -51
AGTCACCACTGACCGGGTCATCTGGAGCCCGTGGCAGGCCGAGGCCCAGG -1
ATGAGGCGCTGGAAGGCAGCGGCCCTGGTGTCGCTCATCTGCAGCTCCCT 50
GCTATCTGTCTGGATGTGCCAGGAGGGTCTGCTCTTGGGCCACCGCCTGG 100
GACCCGCGCTTGCCCCGCTACGACGCCCTCCACGCACCCTGGACGCCCGC 150
ATCGCCCGCCTGGCCCAGTATCGCGCTCTGCTCCAGGGCGCCCCCGACGC 200
GGTGGAGCTTCGAGAACTTTCTCCCTGGGCTGCCCGCATCCCGGGACCGC 250
GCCGTCGAGCGGGTCCCCGGCGTCGGCGGGCGCGGCCGGGGGCTCGGCCT 300
TGTGGGCTGCGCGAGCTCGAGGTGCGCGTGAGCGAGCTGGGCCTGGGCTA 350
CACGTCGGATGAGACCGTGCTGTTCCGCTACTGCGCAGGCGCGTGCGAGG 400
CGGCCATCCGCATCTACGACCTGGGCCTTCGGCGCCTGCGCCAGCGGAGG 450
CGCGTGCGCAGAGAGCGGGCGCGGGCGCACCCGTGTTGTCGCCCGACGGC 500
CTATGAGGACGAGGTGTCCTTCCTGGACGTGCACAGCCGCTACCACACGC 550
TGCAAGAGCTGTCGGCGCGGGAGTGCGCGTGCGTGTGATGCTACCTCACG 600
CCCCCCGACCTGCGAAAGGGCCCTCCCTGCCGACCCTCGCTGAGAACTGA 650
CTTCACATAAAGTGTGGGAACTCCC 675

Figure 9

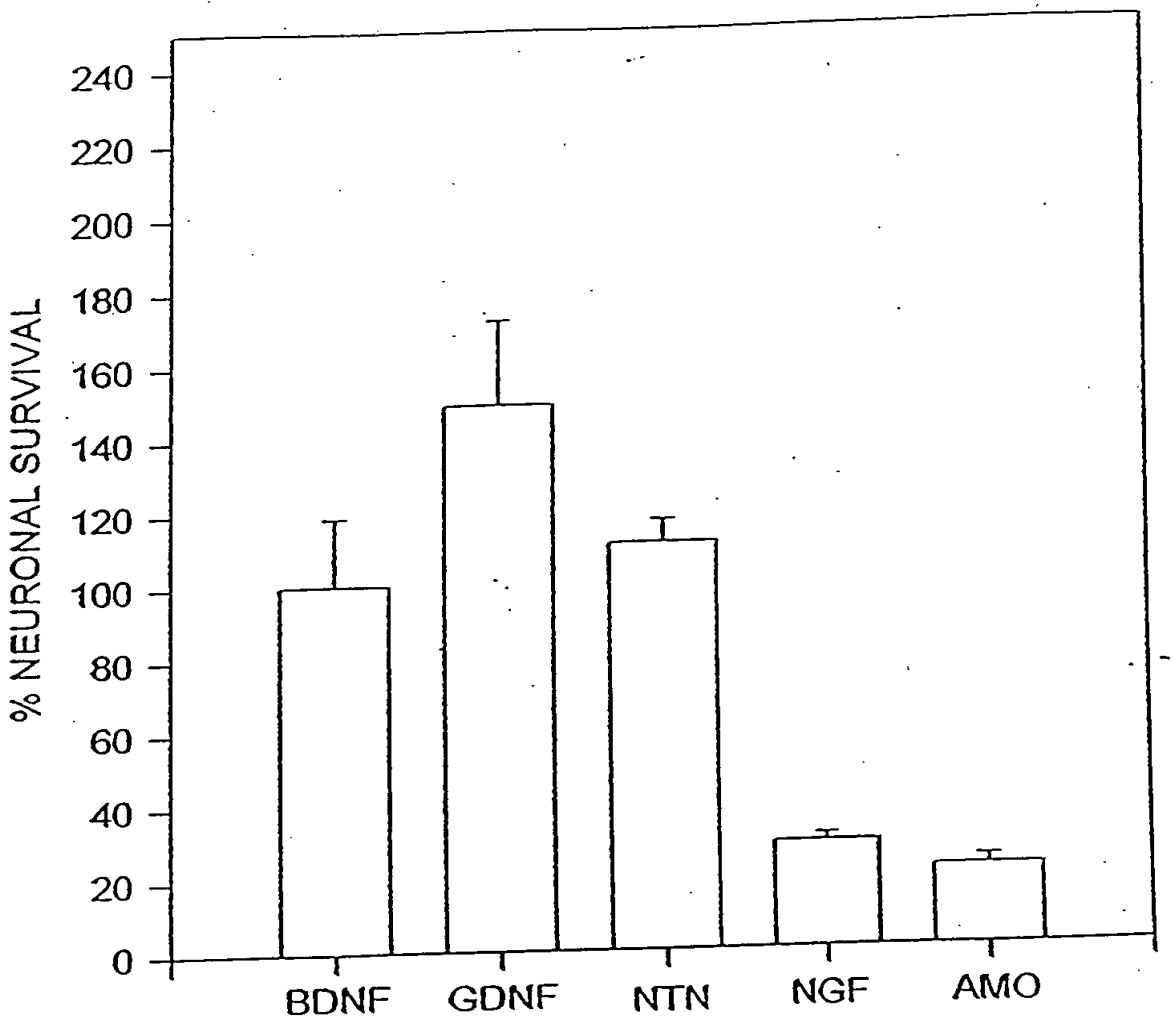

Figure 10

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Glu Gly Pro Gly Arg Pro Ile Arg Val Arg Ile Pro Gly Gly Leu Pro Thr Pro Gln Phe 20

CTTCTCTCAAAGCCCTCACTTTGCCTTACAATCCTACTCTACCTTGCACTAGGTAACAAC 120
Leu Leu Ser Lys Pro Ser Leu Cys Leu Thr Ile Leu Leu Tyr Leu Ala Leu Gly Asn Asn 40

CATGTCCGTCTTCCAAGAGCCTTGGCTGGTTCATGCCGACTGTGGAGCCTGACCCTACCA 180
His Val Arg Leu Pro Arg Ala Leu Ala Gly Ser Cys Arg Leu Trp Ser Leu Thr Leu Pro 60

GTGGCTGAGCTGGGCCTGGGCTATGCCTCGGAGGAGAAGGTCATCTTCCGATACTGTGCT 240
Val Ala Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala 80

GGCAGCTGTCCCCAAGAGGCCCGTACCCAGCACAGTCTGGTACTGGCCCGGCTTCGAGGG 300
Gly Ser Cys Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg Gly 100

CGGGGTCGAGCCCATGGCCGACCCTGCTGCCAGCCCACCAGCTATGCTGATGTGACCTTC 360
Arg Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe 120

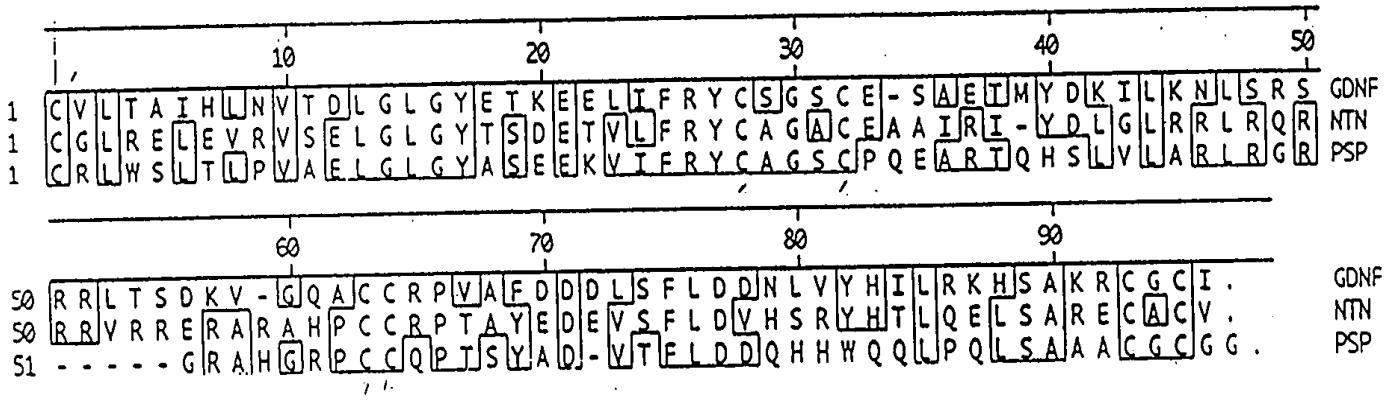
CTTGATGATCAGCACCATTGGCAGCAGCTGCCTCAGCTCTCAGCTGCAGCTTGTGGCTGT 420
Leu Asp Asp Gln His His Trp Gln Gln Leu Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys 140

GGTGGCTGAAGGAGGCCAGTCTGGTGTCTCAGAATCACAAGCATGAGACAGGCTGGGCTT 480
Gly Gly 142

TGAAAGGCTCAGGTGACATTACTAGAAATTTGCATAGGTAAAGATAAGAAGGGAAAGGAC 540

CAGG 544

Figure 11


10
20
30
40
50
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1 C G L R E L E V R V S E L G L G Y T S D E T V L F R Y C A G A C E A A I R I - Y D L G L R R L R Q R NTN
1 C R L W S L T L P V A E L G L G Y A S E E K V I F R Y C A G S C P Q E A R T Q H S L V L A R L R G R PSP
60
70
80
90
50 R R L T S D K V - G Q A C C R P V A F D D D L S F L D D N L V Y H I L R K H S A K R C G C I . GDNF
50 R R V R R E R A R A H P C C R P T A Y E D E V S F L D V H S R Y H T L Q E L S A R E C A C V . NTN
51 - - - - - G R A H G R P C C Q P T S Y A D - V T F L D D Q H H W Q Q L P Q L S A A A C G C G G . PSP

Figure 12

CCTCAGAGGAGAAGATTATCTTCCGATACTGTGCTGGCAGCTGTCCCCAAGAGGTCCGTACC 62
Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser Cys Pro Gln Glu Val Arg Thr 20

CAGCACAGTCTGGTGCTGGCCCGTCTTCGAGGGCAGGGTCGAGCTCATGGCAGACCTTGC 122
Gln His Ser Leu Val Leu Ala Arg Leu Arg Gly Gln Gly Arg Ala His Gly Arg Pro Cys 40

TGCCAGCCCACCAGCTATGCTGATGTGACCTTCCTTGATGACCACCACCATTGGCAGCAG 182
Cys Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp His His His Trp Gln Gln 60

CTGCCTCAGCTCTCAGCCGCAGCTTGTGGCTGTGGTGGCTGAAGGCGGCCAGCCTGGTCT 242
Leu Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly 73

CTCAGAATCACAAGCAAGAGGCAGCCTTTGAAAGGCTCAGGTGACGTTATTAGAAACTTG 302

CATAGGAGAAGATTAAGAAGAGAAAGGGGACCTG 336

Figure 13

TGCCGGCTGTGGAGCCTGACCCTACCAGTGGCTGAGCTTGGCCTGGGCTATGCCTCAGAG 60
Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu Gly Tyr Ala Ser Glu 20

GAGAAGATTATCTTCCGATACTGTGCTGGCAGCTGTCCCCAAGAGGTCCGTACCCAGCAC 120
Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser Cys Pro Gln Glu Val Arg Thr Gln His 40

AGTCTGGTGCTGGCCCGTCTTCGAGGGCAGGGTCGAGCTCATGGCAGACCTTGCTGCCAG 180
Ser Leu Val Leu Ala Arg Leu Arg Gly Gln Gly Arg Ala His Gly Arg Pro Cys Cys Gln 60

CCCACCAGCTATGCTGATGTGACCTTCCTTGATGACCACCACCATTGGCAGCAGCTGCCT 240
Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu Pro 80

CAGCTCTCAGCCGCAGCTTGTGGCTGTGGTGGCTGAAGGCGGCCAGCCTGGTCTCTCAGA 300
Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly 91

ATCACAAGCAAGAGGCAGCCTTTGAAAGGCTCAGGTGACGTTATTAGAAACTTGCATAGG 360

AGAAGATTAAGAAGAGAAAGGGGACCTGATT 391

Figure 14

```
                   10        20        30        40
1  C V L T A I H L N V T D L G L G Y E T K E E L I F R Y C S G S C D A A E T T - Y  GDNF(human)
1  C V L T A I H L N V T D L G L G Y E T K E E L I F R Y C S G S C E A A E T M - Y  GDNF(rat)
1  C V L T A I H L N V T D L G L G Y E T K E E L I F R Y C S G S C E S A E T M - Y  GDNF(mouse)
1  C G L R E L E V R V S E L G L G Y A S D E T V L F R Y C A G A C E A A A R V - Y  NTN(human)
1  C G L R E L E V R V S E L G L G Y T S D E T V L F R Y C A G A C E A A I R I - Y  NTN(mouse)
1  C R L W S L T L P V A E L G L G Y A S E E K I I F R Y C A G S C P Q E V R T Q H  PSP(rat)
1  C R L W S L T L P V A E L G L G Y A S E E K V I F R Y C A G S C P Q E A R T Q H  PSP(mouse)

                   50        60        70        80
40 D K I L K N L S R N R R L V S D K V - G Q A C C R P I A F D D D L S F L D D N L  GDNF(human)
40 D K I L K N L S R S R R L T S D K V - G Q A C C R P V A F D D D L S F L D D S L  GDNF(rat)
40 D K I L K N L S R S R R L T S D K V - G Q A C C R P V A F D D D L S F L D D N L  GDNF(mouse)
40 D L G L R R L R Q R R R L R R E R V R A Q P C C R P T A Y E D E V S F L D A H S  NTN(human)
40 D L G L R R L R Q R R R V R R E R A R A H P C C R P T A Y E D E V S F L D V H S  NTN(mouse)
41 S L V L A R L R - - - - - G Q G R A H G R P C C Q P T S Y A D - V T F L D D H H  PSP(rat)
41 S L V L A R L R - - - - - G R G R A H G R P C C Q P T S Y A D - V T F L D D Q H  PSP(mouse)

                   90
79 V Y H I L R K H S A K R C G C .   GDNF(human)
79 V Y H I L R K H S A K R C G C .   GDNF(rat)
79 V Y H I L R K H S A K R C G C .   GDNF(mouse)
80 R Y H T V H E L S A R E C A C .   NTN(human)
80 R Y H T L Q E L S A R E C A C .   NTN(mouse)
75 H W Q Q L P Q L S A A A C G C .   PSP(rat)
75 H W Q Q L P Q L S A A A C G C .   PSP(mouse)
```

Figure 15 A

```
                    10                  20                  30
 1  A L A G S C R L W S L T L P V A E L G L G Y A S E E K V I F    mPSP
 1  A L P G L C R L W S L T L P V A E L G L G Y A S E E K I I F    rPSP
 1  A L S G P C Q L W S L T L S V A E L G L G Y A S E E K V I F    hPSP

                    40                  50                  60
31  R Y C A G S C P Q E A R T Q H S L V L A R L R G R G R A H G    mPSP
31  R Y C A G S C P Q E V R T Q H S L V L A R L R G Q G R A H G    rPSP
31  R Y C A G S C P Q E V R T Q H S L V L A R L R G Q G R A H G    hPSP
31  R Y C A G S C P R G A R T Q H G L A L A R L Q G Q G R A H G    hPSP

                    70                  80                  90
61  R P C C Q P T S Y A D V T F L D D Q H H W Q Q L P Q L S A A    mPSP
61  R P C C Q P T S Y A D V T F L D D H H H W Q Q L P Q L S A A    rPSP
61  R P C C Q P T S Y A D V T F L D D H H H W Q Q L P Q L S A A    hPSP
61  G P C C R P T R Y T D V A F L D D R H R W Q R L P Q L S A A    hPSP

                                                                 rPSP
91  A C G C G G                                                  rPSP
91  A C G C G G                                                  hPSP
91  A C G C G G                                                  hPSP
```

Figure 15B

	GROWTH FACTOR	SEQUENCE
0	TGFß1	CCVRQLYIDFRKDLGWK-WIHEPKGYHANFCLGPCPYIWSLDT-------QYSKVLALYNQHNPGASAA-PCCV--PQALEPLPIVYYVGRKPKV--EQLSNMIVRSCKCS
1	TGFß2	CCLRPLYIDFKRDLGWK-WIHEPKGYNANFCAGACPYLWSSDT-------QHSRVLSLYNTINPEASAS-PCCV--SQDLEPLTILYYIGKTPKI--EQLSNMIVKSCKCS
2	TGFß3	CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSADT-------THSTVLGLYNTLNPEASAS-PCCV--PQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKCS
3	INHßA	CCKKQFFVSFK-DIGWNDWIIAPSGYHANYCEGECPSHIAG-TSGSSLSFHSTVINHYRMRGHSPFANLKSCCV--PTKLRPMSMLYYDDGQNII-KKDIQNMIVEECGCS
4	INHßB	CCRQQFFIDFR-LIGWNDWIIAPTGYYGNYCEGSCPAYLAG-VPGSASSFHTAVVNQYRMRGLNP-GTVNSCCI--PTKLSTMSMLYFDDEYNIV-KRDVPNMIVEECGCA
5	NODAL	CRRVKFQVDFN-LIGWGSWIIYPKQYNAYRCEGECPNPVGEEFHPT----NHAYIQSLLKRYQPHR-VPSTCCA--PVKTKPLSMLYVDNGR--VLLEHHKDMIVEECGCL
6	BMP2	CKRHPLYVDFS-DVGWNDWIVAPPGYHAFYCHGECPFPLADHLNST----NHAIVQTLVNSVNS-K-IPKACCV--PTELSAISMLYLDENEKVVLK-NYQDMVVEGCGCR
7	BMP4	CRRHSLYVDFS-DVGWNDWIVAPPGYQAFYCHGDCPFPLADHLNST----NHAIVQTLVNSVNS-S-IPKACCV--PTELSAISMLYLDEYDKVVLK-NYQEMVVEGCGCR
8	DPP	CRRHSLYVDFS-DVGWDDWIVAPLGYDAYYCHGKCPFPLADHFNST----NHAVVQTLVNNMNPGK-VPKACCV--PTQLDSVAMLYLNDQSTVVLK-NYQEMTVVGCGCR
9	BMP5	CKKHELYVSFR-DLGWQDWIIAPEGYAAFYCDGECSFPLNAHMNAT----NHAIVQTLVHLMFPDH-VPKPCCA--PTKLNAISVLYFDDSSNVILK-KYRNMVVRSCGCH
10	BMP6	CRKHELYVSFQ-DLGWQDWIIAPKGYAANYCDGECSFPLNAHMNAT----NHAIVQTLVHLMNPEY-VPKPCCA--PTKLNAISVLYFDDNSNVILK-KYRNMVVRACGCH
11	BMP7	CKKHELYVSFR-DLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNAT----NHAIVQTLVHFINPET-VPKPCCA--PTQLNAISVLYFDDSSNVILK-KYRNMVVRACGCH
12	BMP8	CRRHELYVSFQ-DLGWLDWVIAPQGYSAYYCEGECSFPLDSCMNAT----NHAILQSLVHLMKPNA-VPKACCA--PTKLSATSVLYYDSSNNVILR-KHRNMVVKACGCH
13	60A	CQMQTLYIDFK-DLGWHDWIIAPEGYGAFYCSGECNFPLNAHMNAT----NHAIVQTLVHLLEPKK-VPKPCCA--PTRLGALPVLYHLNDENVNLK-KYRNMIVKSCGCH
14	BMP3	CARRYLKVDFA-DIGWSEWIISPKSFDAYYCSGACQFPMPKSLKPS----NHATIQSIVRAVGVVPGIPEPCCV--PEKMSSLSILFFDENKNVVLKV-YPNMTVESCACR
15	VG1	CKKRHLYVEFK-DVGWQNWVIAPQGYMANYCYGECPYPLTEILNGS----NHAILQTLVHSIEPED-IPLPCCV--PTKMSPISMLFYDNNDNVVLR-HYENMAVDECGCR
16	GDF1	CRARRLYVSFR-EVGWHRWVIAPRGFLANYCQGQCALPVALSGSGGPPALNHAVLRALMHAAAPGA-ADLPCCV--PARLSPISVLFFDNSDNVVLR-QYEDMVVDECGCR
17	GDF3	CHRHQLFINFQ-DLGWHKWVIAPKGFMANYCHGECPFSMTTYLNSS----NYAFMQALMHMADP-K-VPKAVCV--PTKLSPISMLYQDSDKNVILR-HYEDMVVDECGCG
18	DORSLN	CRRTSLHVNFK-EIGWDSWIIAPKDYEAFECKGGCFFPLTDNVTPT----KHAIVQTLVHLQNPKK-ASKACCV--PTKLDAISILYKDDAGVPTLIYNYEGMKVAECGCR
19	INHα	CHRVALNISF-QELGWERWIVYPPSFIFHYCHGGCGLHIPPNLSLPVPGAPPTPAQPYSLL-----PGAQPCCAALPGTMRPLHVRTTSDGGYSFKYETVPNLLTQHCACI
20	MIS	CALRELSVDLRAERS----VLIPETYQAANNCQGACGWPQSDR----NPRYGNHVVLLLKMQARGATLARPPCCV--PTAYT--GKLLISLSEERISAHHVPNMVATECGCR
21	GDF9	CELHDFSLSFS-QLKWDNWIVAPHSYNPSYCKGDCPSAVSHRYGSPV----HTMVQNMIYE-KLDPSVPSPSCV--PGKYSPLSVLTIEPDGSIAYK-EYEDMMATSCTCR
22	GDNF	CVLTAIHLNVT-DLGLG--YETKEELIFRYCSGSCD-AAETTYDKILKNLSRN------RRLVSDKV-GQACCRPIAFD-DDLSFL-----DDNLVYHILRKHSAKRCGCI
23	NTN	CGLRELEVRVS-ELGLG--YASDETVLFRYCAGACE-AAARVYDLGLRRLRQR------RRLRRERVRAQPCCRPTAYE-DEVSFL-----DAHSRYHTVHELSARECACV

FIGURE 16

```
1    ATGGCTGCAG GAAGACTTCG GATCCTGTGT CTGCTGCTCC TGTCCTTGCA CCCGAGCCTC
     TACCGACGTC CTTCTGAAGC CTAGGACACA GACGACGAGG ACAGGAACGT GGGCTCGGAG

61   GGCTGGGTCC TTGATCTTCA AGAGGCTTCT GTGGCAGATA AGCTCTCATT TGGGAAGATG
     CCGACCCAGG AACTAGAAGT TCTCCGAAGA CACCGTCTAT TCGAGAGTAA ACCCTTCTAC

121  GCAGAGACTA GAGGGACCTG GACGCCCCAT CAGGGTAAGA ATTCCTGGGG GCCTCCCGAC
     CGTCTCTGAT CTCCCTGGAC CTGCGGGGTA GTCCCATTCT TAAGGACCCC CGGAGGGCTG

181  TCCCCAATTC CTTCTCTCAA AGCCCTCACT TTGCCTTACA ATCCTACTCT ACCTTGCACT
     AGGGGTTAAG GAAGAGAGTT TCGGGAGTGA AACGGAATGT TAGGATGAGA TGGAACGTGA

241  AGGTAACAAC CATGTCCGTC TTCCAAGAGC CTTGGCTGGT TCATGCCGAC TGTGGAGCCT
     TCCATTGTTG GTACAGGCAG AAGGTTCTCG GAACCGACCA AGTACGGCTG ACACCTCGGA

301  GACCCTACCA GTGGCTGAGC TGGGCCTGGG CTATGCCTCG GAGGAGAAGG TCATCTTCCG
     CTGGGATGGT CACCGACTCG ACCCGGACCC GATACGGAGC CTCCTCTTCC AGTAGAAGGC

361  ATACTGTGCT GGCAGCTGTC CCCAAGAGGC CCGTACCCAG CACAGTCTGG TACTGGCCCG
     TATGACACGA CCGTCGACAG GGGTTCTCCG GGCATGGGTC GTGTCAGACC ATGACCGGGC

421  GCTTCGAGGG CGGGGTCGAG CCCATGGCCG ACCCTGCTGC CAGCCCACCA GCTATGCTGA
     CGAAGCTCCC GCCCCAGCTC GGGTACCGGC TGGGACGACG GTCGGGTGGT CGATACGACT

481  TGTGACCTTC CTTGATGATC AGCACCATTG GCAGCAGCTG CCTCAGCTCT CAGCTGCAGC
     ACACTGGAAG GAACTACTAG TCGTGGTAAC CGTCGTCGAC GGAGTCGAGA GTCGACGTCG

541  TTGTGGCTGT GGTGGCTGAA GGAGGCCAGT CTGGTGTCTC AGAATCACAA GCATGAGACA
     AACACCGACA CCACCGACTT CCTCCGGTCA GACCACAGAG TCTTAGTGTT CGTACTCTGT

601  GGCTGGGCTT TGAAAGGCTC AGGTGACATT ACTAGAAATT TGCATAGGTA AAGATAAGAA
     CCGACCCGAA ACTTTCCGAG TCCACTGTAA TGATCTTTAA ACGTATCCAT TTCTATTCTT

661  GGGAAAGGAC CAGGGGTTTT TTGTTTCTTT CTTTGCTTGC TTGTTAGTTT TTTTTTTTTT
     CCCTTTCCTG GTCCCCAAAA AACAAAGAAA GAAACGAACG AACAATCAAA AAAAAAAAAA

721  TTT
     AAA
```

Figure 17A

```
   1  ATGGCTGCAG GAAGACTTCG GATCCTGTGT CTGCTGCTCC TGTCCTTGCA CCCGAGCCTC
      TACCGACGTC CTTCTGAAGC CTAGGACACA GACGACGAGG ACAGGAACGT GGGCTCGGAG
   1  M  A  A  G    R  L  R    I  L  C    L  L  L  L    S  L  H    P  S  L

  61  GGCTGGGTCC TTGATCTTCA AGAGGCTTCT GTGGCAGATA AGCTCTCATT TGGGAAGATG
      CCGACCCAGG AACTAGAAGT TCTCCGAAGA CACCGTCTAT TCGAGAGTAA ACCCTTCTAC
  21  G  W  V  L    D  L  Q    E  A  S    V  A  D  K    L  S  F    G  K  M
                                                 ↓
 121  GCAGAGACTA GAGGGACCTG GACGCCCCAT CAGGGTAACA ACCATGTCCG TCTTCCAAGA
      CGTCTCTGAT CTCCCTGGAC CTGCGGGGTA GTCCCATTGT TGGTACAGGC AGAAGGTTCT
  41  A  E  T  R    G  T  W    T  P  H    Q  G  N  N    H  V  R    L  P  R

 181  GCCTTGGCTG GTTCATGCCG ACTGTGGAGC CTGACCCTAC CAGTGGCTGA GCTGGGCCTG
      CGGAACCGAC CAAGTACGGC TGACACCTCG GACTGGGATG GTCACCGACT CGACCCGGAC
  61  A  L  A  G    S  C  R    L  W  S    L  T  L  P    V  A  E    L  G  L

 241  GGCTATGCCT CGGAGGAGAA GGTCATCTTC CGATACTGTG CTGGCAGCTG TCCCCAAGAG
      CCGATACGGA GCCTCCTCTT CCAGTAGAAG GCTATGACAC GACCGTCGAC AGGGGTTCTC
  81  G  Y  A  S    E  E  K    V  I  F    R  Y  C  A    G  S  C    P  Q  E

 301  GCCCGTACCC AGCACAGTCT GGTACTGGCC CGGCTTCGAG GGCGGGGTCG AGCCCATGGC
      CGGGCATGGG TCGTGTCAGA CCATGACCGG GCCGAAGCTC CCGCCCCAGC TCGGGTACCG
 101  A  R  T  Q    H  S  L    V  L  A    R  L  R  G    R  G  R    A  H  G

 361  CGACCCTGCT GCCAGCCCAC CAGCTATGCT GATGTGACCT TCCTTGATGA TCAGCACCAT
      GCTGGGACGA CGGTCGGGTG GTCGATACGA CTACACTGGA AGGAACTACT AGTCGTGGTA
 121  R  P  C  C    Q  P  T    S  Y  A    D  V  T  F    L  D  D    Q  H  H

 421  TGGCAGCAGC TGCCTCAGCT CTCAGCTGCA GCTTGTGGCT GTGGTGGCTG A
      ACCGTCGTCG ACGGAGTCGA GAGTCGACGT CGAACACCGA CACCACCGAC T
 141  W  Q  Q  L    P  Q  L    S  A  A    A  C  G  C    G  G  .
```

Figure 17B

```
1   ATGGCTGCAG GAAGACTTCG GATCTTGTTT CTGCTGCTCC TGTCCTTGCA CCTGGGCCTT
    TACCGACGTC CTTCTGAAGC CTAGAACAAA GACGACGAGG ACAGGAACGT GGACCCGGAA

61  GGCTGGGTCC TTGATCTTCA AGAGGCTCCT GCGGCAGATG AGCTCTCATC TGGGAAAATG
    CCGACCCAGG AACTAGAAGT TCTCCGAGGA CGCCGTCTAC TCGAGAGTAG ACCCTTTTAC

121 GCAGAGACTG GAAGGACCTG GAAGCCCCAT CAGGGTAAGA ATTCTTGGGG GCCTCCTAAC
    CGTCTCTGAC CTTCCTGGAC CTTCGGGGTA GTCCCATTCT TAAGAACCCC CGGAGGATTG

181 TCTACAGTTC TTCCTCTCAA AGCCCTCACT TTGCCTCACA ATCCTATTCT ACCTTGCACT
    AGATGTCAAG AAGGAGAGTT TCGGGAGTGA AACGGAGTGT TAGGATAAGA TGGAACGTGA

241 AGGTAACAAC AATGTCCGCC TTCCAAGAGC CTTACCTGGT TTGTGCCGGC TGTGGAGCCT
    TCCATTGTTG TTACAGGCGG AAGGTTCTCG GAATGGACCA AACACGGCCG ACACCTCGGA

301 GACCCTACCA GTGGCTGAGC TTGGCCTGGG CTATGCCTCA GAGGAGAAGA TTATCTTCCG
    CTGGGATGGT CACCGACTCG AACCGGACCC GATACGGAGT CTCCTCTTCT AATAGAAGGC

361 ATACTGTGCT GGCAGCTGTC CCCAAGAGGT CCGTACCCAG CACAGTCTGG TGCTGGCCCG
    TATGACACGA CCGTCGACAG GGGTTCTCCA GGCATGGGTC GTGTCAGACC ACGACCGGGC

421 TCTTCGAGGG CAGGGTCGAG CTCATGGCAG ACCTTGCTGC CAGCCCACCA GCTATGCTGA
    AGAAGCTCCC GTCCCAGCTC GAGTACCGTC TGGAACGACG GTCGGGTGGT CGATACGACT

481 TGTGACCTTC CTTGATGACC ACCACCATTG GCAGCAGCTG CCTCAGCTCT CAGCCGCAGC
    ACACTGGAAG GAACTACTGG TGGTGGTAAC CGTCGTCGAC GGAGTCGAGA GTCGGCGTCG

541 TTGTGGCTGT GGTGGCTGA
    AACACCGACA CCACCGACT
```

Figure 18A

```
   1  ATGGCTGCAG GAAGACTTCG GATCTTGTTT CTGCTGCTCC TGTCCTTGCA CCTGGGCCTT
      TACCGACGTC CTTCTGAAGC CTAGAACAAA GACGACGAGG ACAGGAACGT GGACCCGGAA
   1  M  A  A  G    R  L  R    I  L  F    L  L  L  L    S  L  H    L  G  L

  61  GGCTGGGTCC TTGATCTTCA AGAGGCTCCT GCGGCAGATG AGCTCTCATC TGGGAAAATG
      CCGACCCAGG AACTAGAAGT TCTCCGAGGA CGCCGTCTAC TCGAGAGTAG ACCCTTTTAC
  21  G  W  V  L    D  L  Q    E  A  P    A  A  D  E    L  S  S    G  K  M

 121  GCAGAGACTG GAAGGACCTG GAAGCCCCAT CAGGGTAACA ACAATGTCCG CCTTCCAAGA
      CGTCTCTGAC CTTCCTGGAC CTTCGGGGTA GTCCCATTGT TGTTACAGGC GGAAGGTTCT
  41  A  E  T  G    R  T  W    K  P  H    Q  G  N  N    N  V  R    L  P  R

 181  GCCTTACCTG GTTTGTGCCG GCTGTGGAGC CTGACCCTAC CAGTGGCTGA GCTTGGCCTG
      CGGAATGGAC CAAACACGGC CGACACCTCG GACTGGGATG GTCACCGACT CGAACCGGAC
  61  A  L  P  G    L  C  R    L  W  S    L  T  L  P    V  A  E    L  G  L

 241  GGCTATGCCT CAGAGGAGAA GATTATCTTC CGATACTGTG CTGGCAGCTG TCCCCAAGAG
      CCGATACGGA GTCTCCTCTT CTAATAGAAG GCTATGACAC GACCGTCGAC AGGGGTTCTC
  81  G  Y  A  S    E  E  K    I  I  F    R  Y  C  A    G  S  C    P  Q  E

 301  GTCCGTACCC AGCACAGTCT GGTGCTGGCC CGTCTTCGAG GGCAGGGTCG AGCTCATGGC
      CAGGCATGGG TCGTGTCAGA CCACGACCGG GCAGAAGCTC CCGTCCCAGC TCGAGTACCG
 101  V  R  T  Q    H  S  L    V  L  A    R  L  R  G    Q  G  R    A  H  G

 361  AGACCTTGCT GCCAGCCCAC CAGCTATGCT GATGTGACCT TCCTTGATGA CCACCACCAT
      TCTGGAACGA CGGTCGGGTG GTCGATACGA CTACACTGGA AGGAACTACT GGTGGTGGTA
 121  R  P  C  C    Q  P  T    S  Y  A    D  V  T  F    L  D  D    H  H  H

 421  TGGCAGCAGC TGCCTCAGCT CTCAGCCGCA GCTTGTGGCT GTGGTGGCTG A
      ACCGTCGTCG ACGGAGTCGA GAGTCGGCGT CGAACACCGA CACCACCGAC T
 141  W  Q  Q  L    P  Q  L    S  A  A    A  C  G  C    G  G  .
```

Figure 18B

Figure 19

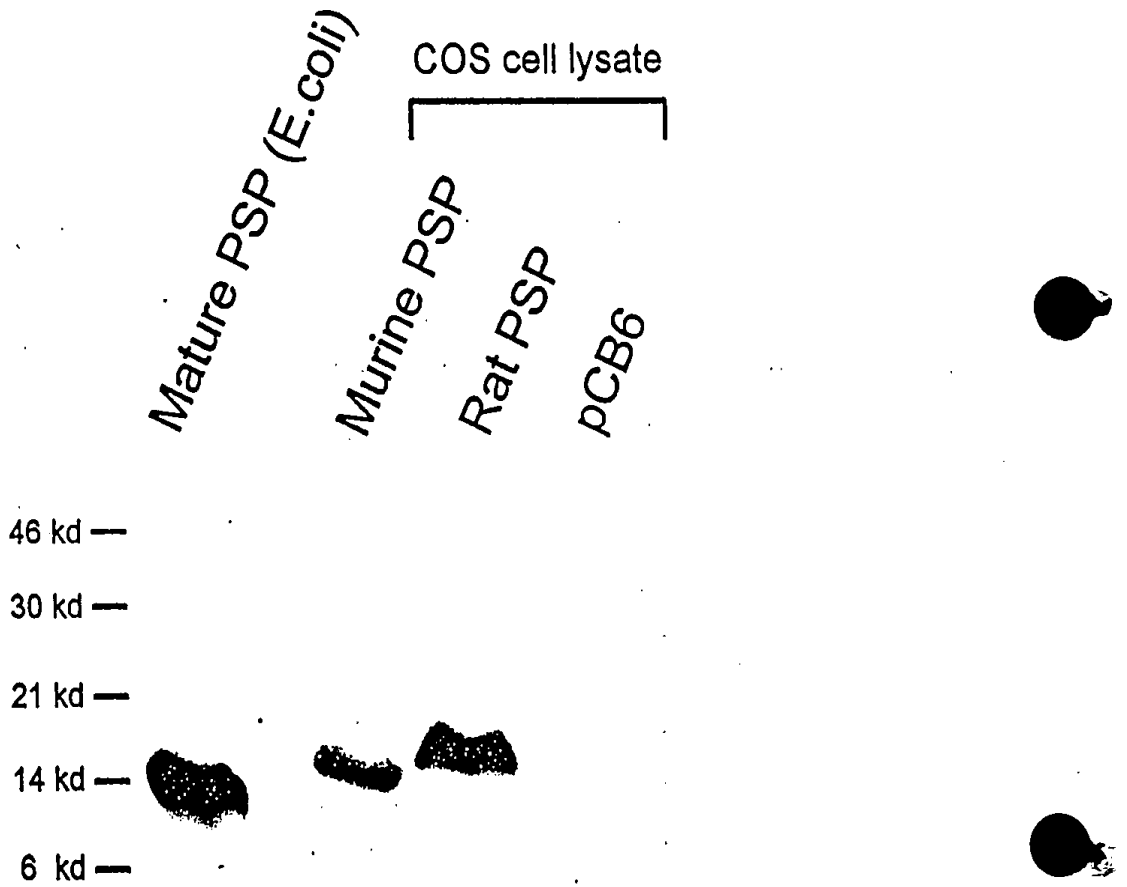

Mature PSP (E.coli)
COS cell lysate
Murine PSP
Rat PSP
pCB6
46 kd
30 kd
21 kd
14 kd
6 kd

FIGURE 20A

PSP/NTN (SEQ ID NO: 137)

ALAGSCRLWSLTLPVAELGLGYASEEKVIFRYCAGSCPQEARTQHSLVLA 50

RLRGRGRAHGRPCCRPTAYEDEVSFLDVHSRYHTLQELSARECACV 96

FIGURE 20B

NTN/PSP (SEQ ID NO: 142)

PGARPCGLRELEVRVSELGLGYTSDETVLFRYCAGACEAAIRIYDLGLRR 50

LRQRRRVRRERARAHPCCQPTSYADVTFLDDQHHWQQLPQLSAAACGCGG 100

Figure 21a

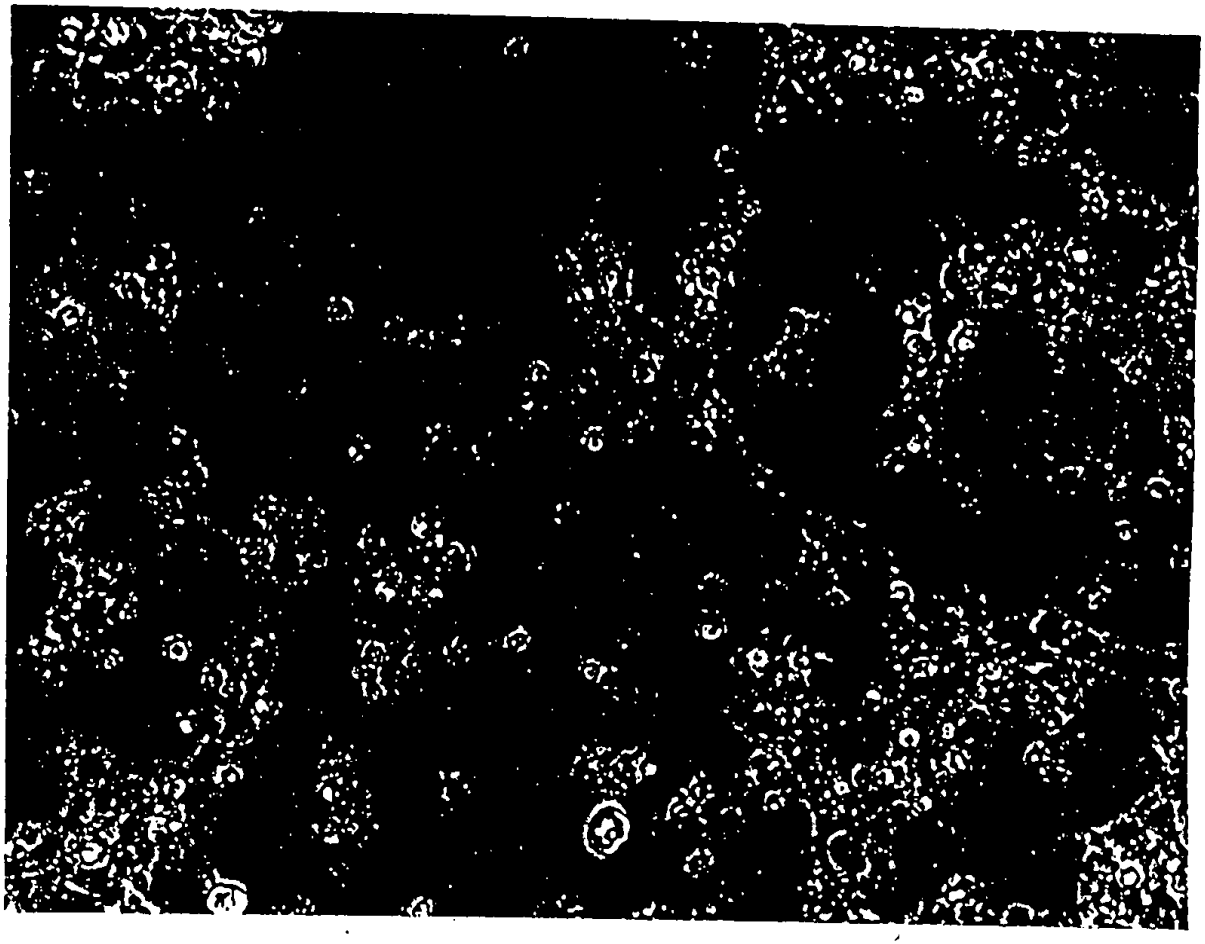
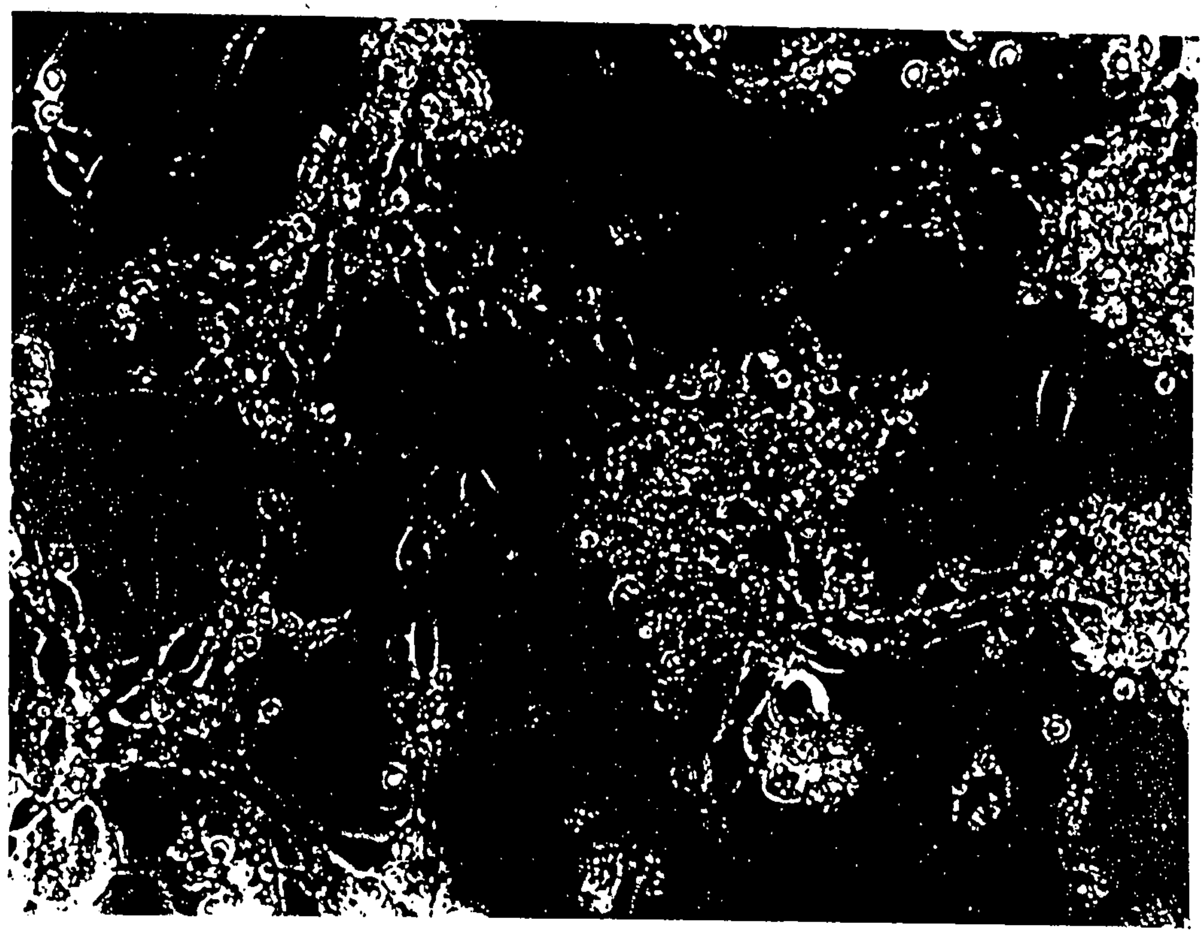


Figure 21b



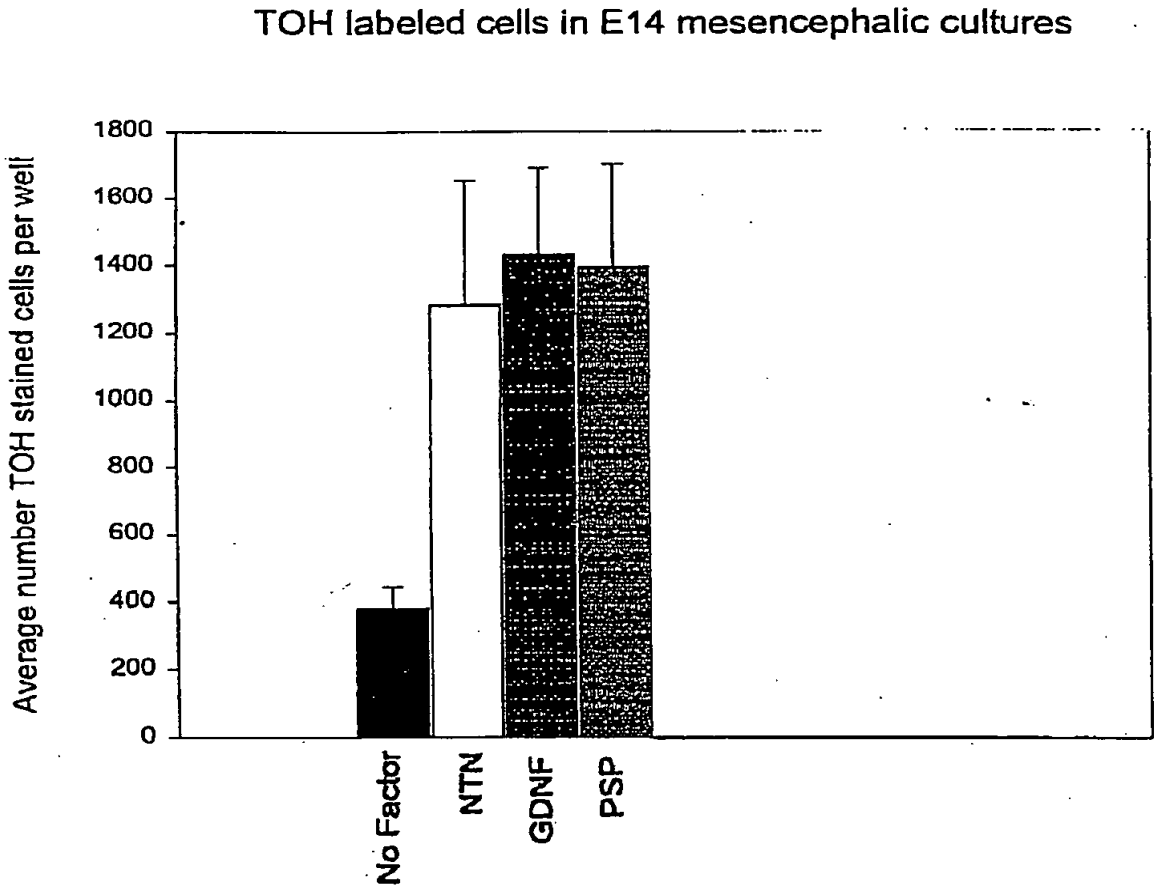


Figure 22

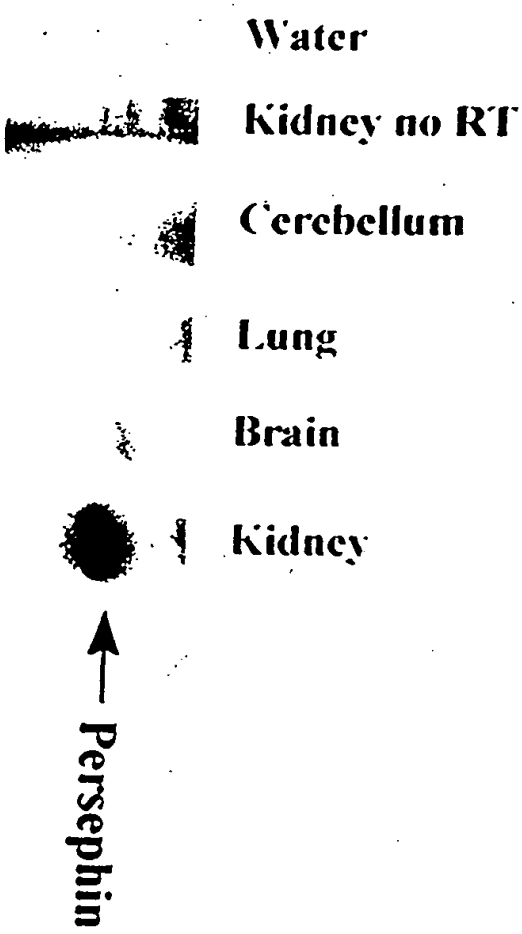


Figure 23

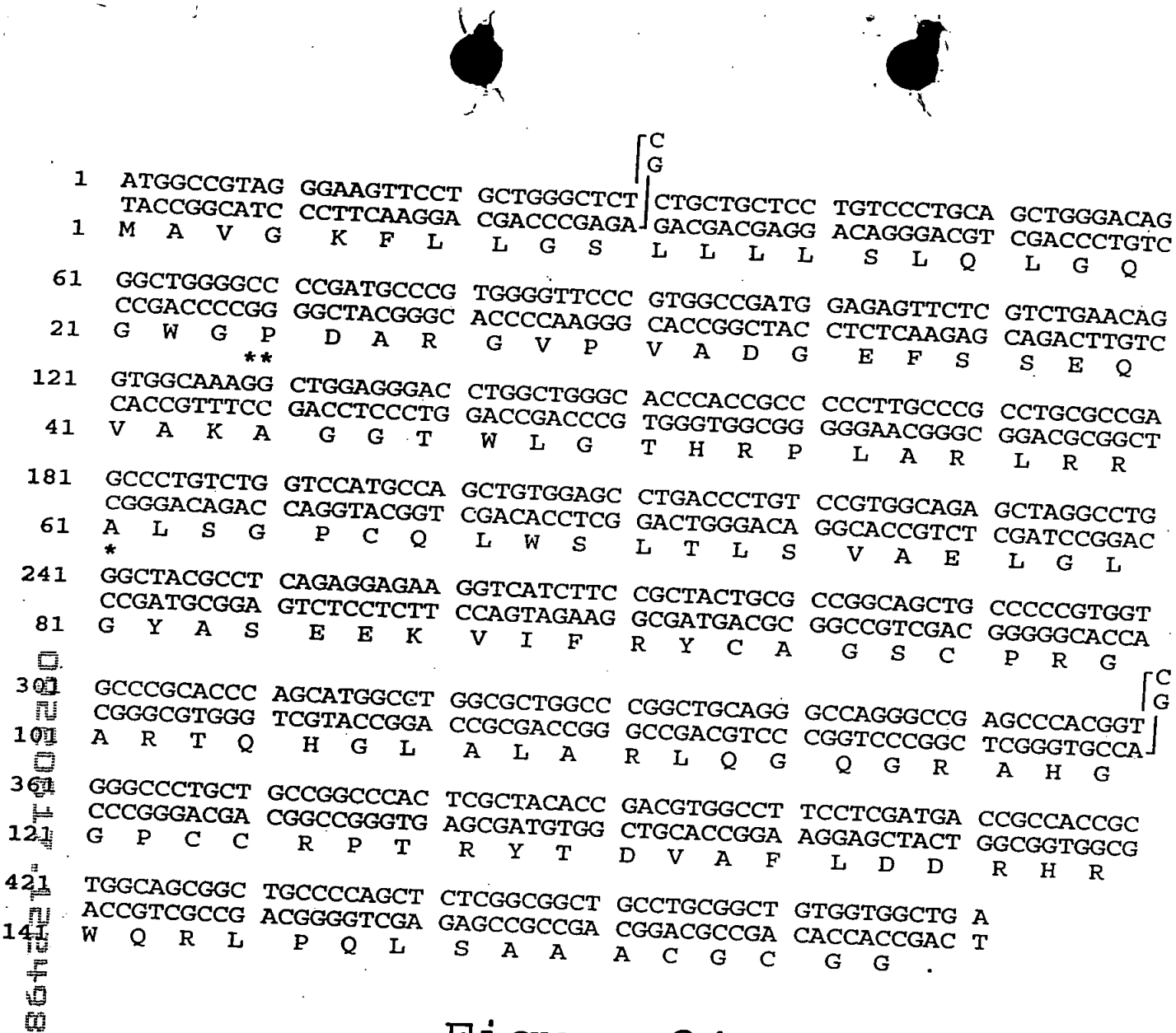

1 ATGGCCGTAG GGAAGTTCCT GCTGGGCTCT CTGCTGCTCC TGTCCCTGCA GCTGGGACAG
TACCGGCATC CCTTCAAGGA CGACCCGAGA GACGACGAGG ACAGGGACGT CGACCCTGTC
1 M A V G K F L L G S L L L L S L Q L G Q
61 GGCTGGGGCC CCGATGCCCG TGGGGTTCCC GTGGCCGATG GAGAGTTCTC GTCTGAACAG
CCGACCCCGG GGCTACGGGC ACCCCAAGGG CACCGGCTAC CTCTCAAGAG CAGACTTGTC
21 G W G P D A R G V P V A D G E F S S E Q
**
121 GTGGCAAAGG CTGGAGGGAC CTGGCTGGGC ACCCACCGCC CCCTTGCCCG CCTGCGCCGA
CACCGTTTCC GACCTCCCTG GACCGACCCG TGGGTGGCGG GGGAACGGGC GGACGCGGCT
41 V A K A G G T W L G T H R P L A R L R R
181 GCCCTGTCTG GTCCATGCCA GCTGTGGAGC CTGACCCTGT CCGTGGCAGA GCTAGGCCTG
CGGGACAGAC CAGGTACGGT CGACACCTCG GACTGGGACA GGCACCGTCT CGATCCGGAC
61 A L S G P C Q L W S L T L S V A E L G L
*
241 GGCTACGCCT CAGAGGAGAA GGTCATCTTC CGCTACTGCG CCGGCAGCTG CCCCCGTGGT
CCGATGCGGA GTCTCCTCTT CCAGTAGAAG GCGATGACGC GGCCGTCGAC GGGGGCACCA
81 G Y A S E E K V I F R Y C A G S C P R G
301 GCCCCGCACCC AGCATGGCCT GGCGCTGGCC CGGCTGCAGG GCCAGGGCCG AGCCCACGGT
CGGGGCGTGGG TCGTACCGGA CCGCGACCGG GCCGACGTCC CGGTCCCGGC TCGGGTGCCA
101 A R T Q H G L A L A R L Q G Q G R A H G
361 GGGCCCTGCT GCCGGCCCAC TCGCTACACC GACGTGGCCT TCCTCGATGA CCGCCACCGC
CCCGGGACGA CGGCCGGGTG AGCGATGTGG CTGCACCGGA AGGAGCTACT GGCGGTGGCG
121 G P C C R P T R Y T D V A F L D D R H R
421 TGGCAGCGGC TGCCCCAGCT CTCGGCGGCT GCCTGCGGCT GTGGTGGCTG A
ACCGTCGCCG ACGGGGTCGA GAGCCGCCGA CGGACGCCGA CACCACCGAC T
141 W Q R L P Q L S A A A C G C G G .

Figure 24